

JUN 2002

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P#23 OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/126,816A

DATE: 06/03/2002
TIME: 13:00:21

Input Set : A:\98502bet.app
Output Set: N:\CRF3\06032002\I126816A.raw

3 <110> APPLICANT: VON EICHEL-STREIBER, CHRISTOPH
4 BOQUET, PATRICE
5 THELESTAM, MONICA
7 <120> TITLE OF INVENTION: METHOD OF INACTIVATION OF RAS SUBFAMILY PROTEINS AND
8 AGENTS THEREFOR
10 <130> FILE REFERENCE: 98501/254992/bet
12 <140> CURRENT APPLICATION NUMBER: 09/126,816A
C--> 13 <141> CURRENT FILING DATE: 2002-05-21
15 <150> PRIOR APPLICATION NUMBER: PCT/EP97/00426
16 <151> PRIOR FILING DATE: 1997-01-31
18 <150> PRIOR APPLICATION NUMBER: 96 101 469.3
19 <151> PRIOR FILING DATE: 1996-02-02
21 <160> NUMBER OF SEQ ID NOS: 6
23 <170> SOFTWARE: PatentIn Ver. 2.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 31
27 <212> TYPE: DNA
28 <213> ORGANISM: Artificial Sequence
30 <220> FEATURE:
31 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
33 <400> SEQUENCE: 1
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37 <210> SEQ ID NO: 2
38 <211> LENGTH: 29
39 <212> TYPE: DNA
40 <213> ORGANISM: Artificial Sequence
42 <220> FEATURE:
43 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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46 ttccagataat gtaggtacca agtctatag 29
49 <210> SEQ ID NO: 3
50 <211> LENGTH: 29
51 <212> TYPE: DNA
52 <213> ORGANISM: Artificial Sequence
54 <220> FEATURE:
55 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
57 <400> SEQUENCE: 3
58 ctatagactt ggtacctaca ttatctgaa 29
61 <210> SEQ ID NO: 4
62 <211> LENGTH: 28
63 <212> TYPE: DNA
64 <213> ORGANISM: Artificial Sequence
66 <220> FEATURE:

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67 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 69 <400> SEQUENCE: 4
 70 tattaacgtg ggcccaatat atgtctac 28
 73 <210> SEQ ID NO: 5
 74 <211> LENGTH: 25
 75 <212> TYPE: PRT
 76 <213> ORGANISM: Artificial Sequence
 78 <220> FEATURE:
 79 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 80 peptide
 82 <400> SEQUENCE: 5
 83 Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr
 84 1 5 10 15
 86 Asp Pro Thr Ile Glu Asp Ser Tyr Arg
 87 20 25
 90 <210> SEQ ID NO: 6
 91 <211> LENGTH: 2364
 92 <212> TYPE: PRT
 93 <213> ORGANISM: Clostridium sordellii
 95 <400> SEQUENCE: 6
 96 Met Asn Leu Val Asn Lys Ala Gln Leu Gln Lys Met Val Tyr Val Lys
 97 1 5 10 15
 99 Phe Arg Ile Gln Glu Asp Glu Tyr Val Ala Ile Leu Asn Ala Leu Glu
 100 20 25 30
 102 Glu Tyr His Asn Met Ser Glu Ser Ser Val Val Glu Lys Tyr Leu Lys
 103 35 40 45
 105 Leu Lys Asp Ile Asn Asn Leu Thr Asp Asn Tyr Leu Asn Thr Tyr Lys
 106 50 55 60
 108 Lys Ser Gly Arg Asn Lys Ala Leu Lys Lys Phe Lys Glu Tyr Leu Thr
 109 65 70 75 80
 111 Met Glu Val Leu Glu Leu Lys Asn Asn Ser Leu Thr Pro Val Glu Lys
 112 85 90 95
 114 Asn Leu His Phe Ile Trp Ile Gly Gly Gln Ile Asn Asp Thr Ala Ile
 115 100 105 110
 117 Asn Tyr Ile Asn Gln Trp Lys Asp Val Asn Ser Asp Tyr Thr Val Lys
 118 115 120 125
 120 Phe Val Tyr Asp Ser Asn Ala Phe Leu Ile Asn Thr Leu Lys Lys Thr
 121 130 135 140
 123 Ile Val Glu Ser Ala Thr Asn Asn Thr Leu Glu Ser Phe Arg Glu Asn
 124 145 150 155 160
 126 Leu Asn Asp Pro Glu Phe Asp Tyr Asn Lys Phe Tyr Arg Lys Arg Met
 127 165 170 175
 129 Glu Ile Ile Tyr Asp Lys Gln Lys His Phe Ile Asp Tyr Tyr Lys Ser
 130 180 185 190
 132 Gln Ile Glu Glu Asn Pro Glu Phe Ile Ile Asp Asn Ile Ile Lys Thr
 133 195 200 205
 135 Tyr Leu Ser Asn Glu Tyr Ser Lys Asp Leu Glu Ala Leu Asn Lys Tyr
 136 210 215 220
 138 Ile Glu Glu Ser Leu Asn Lys Ile Thr Ala Asn Asn Gly Asn Asp Ile

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139	225	230	235	240
141	Arg Asn Leu Glu Lys Phe Ala Asp Glu Asp Leu Val Arg Leu Tyr Asn			
142		245	250	255
144	Gln Glu Leu Val Glu Arg Trp Asn Leu Ala Ala Ala Ser Asp Ile Leu			
145		260	265	270
147	Arg Ile Ser Met Leu Lys Glu Asp Gly Gly Val Tyr Leu Asp Val Asp			
148		275	280	285
150	Ile Leu Pro Gly Ile Gln Pro Asp Leu Phe Lys Ser Ile Asn Lys Pro			
151		290	295	300
153	Asp Ser Ile Thr Asn Thr Ser Trp Glu Met Ile Lys Leu Glu Ala Ile			320
154		305	310	315
156	Met Lys Tyr Lys Glu Tyr Ile Pro Gly Tyr Thr Ser Lys Asn Phe Asp			335
157		325	330	
159	Met Leu Asp Glu Glu Val Gln Arg Ser Phe Glu Ser Ala Leu Ser Ser			
160		340	345	350
162	Lys Ser Asp Lys Ser Glu Ile Phe Leu Pro Leu Asp Asp Ile Lys Val			
163		355	360	365
165	Ser Pro Leu Glu Val Lys Ile Ala Phe Ala Asn Asn Ser Val Ile Asn			
166		370	375	380
168	Gln Ala Leu Ile Ser Leu Lys Asp Ser Tyr Cys Ser Asp Leu Val Ile			
169		385	390	395
171	Asn Gln Ile Lys Asn Arg Tyr Lys Ile Leu Asn Asp Asn Leu Asn Pro			
172		405	410	415
174	Ser Ile Asn Glu Gly Thr Asp Phe Asn Thr Thr Met Lys Ile Phe Ser			
175		420	425	430
177	Asp Lys Leu Ala Ser Ile Ser Asn Glu Asp Asn Met Met Phe Met Ile			
178		435	440	445
180	Lys Ile Thr Asn Tyr Leu Lys Val Gly Phe Ala Pro Asp Val Arg Ser			
181		450	455	460
183	Thr Ile Asn Leu Ser Gly Pro Gly Val Tyr Thr Gly Ala Tyr Gln Asp			
184		465	470	475
186	Leu Leu Met Phe Lys Asp Asn Ser Thr Asn Ile His Leu Leu Glu Pro			
187		485	490	495
189	Glu Leu Arg Asn Phe Glu Phe Pro Lys Thr Lys Ile Ser Gln Leu Thr			
190		500	505	510
192	Glu Gln Glu Ile Thr Ser Leu Trp Ser Phe Asn Gln Ala Arg Ala Lys			
193		515	520	525
195	Ser Gln Phe Glu Glu Tyr Lys Lys Gly Tyr Phe Glu Gly Ala Leu Gly			
196		530	535	540
198	Glu Asp Asp Asn Leu Asp Phe Ala Gln Asn Thr Val Leu Asp Lys Asp			
199		545	550	560
201	Tyr Val Ser Lys Lys Ile Leu Ser Ser Met Lys Thr Arg Asn Lys Glu			
202		565	570	575
204	Tyr Ile His Tyr Ile Val Gln Leu Gln Gly Asp Lys Ile Ser Tyr Glu			
205		580	585	590
207	Ala Ser Cys Asn Leu Phe Ser Lys Asp Pro Tyr Ser Ser Ile Leu Tyr			
208		595	600	605
210	Gln Lys Asn Ile Glu Gly Ser Glu Thr Ala Tyr Tyr Tyr Val Ala			
211		610	615	620

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213 Asp Ala Glu Ile Lys Glu Ile Asp Lys Tyr Arg Ile Pro Tyr Gln Ile 640
 214 625 630 635 640
 216 Ser Asn Lys Arg Asn Ile Lys Leu Thr Phe Ile Gly His Gly Lys Ser 655
 217 645 650 655
 219 Glu Phe Asn Thr Asp Thr Phe Ala Asn Leu Asp Val Asp Ser Leu Ser 670
 220 660 665 670
 222 Ser Glu Ile Glu Thr Ile Leu Asn Leu Ala Lys Ala Asp Ile Ser Pro 685
 223 675 680 685
 225 Lys Tyr Ile Glu Ile Asn Leu Leu Gly Cys Asn Met Phe Ser Tyr Ser 700
 226 690 695 700
 228 Ile Tyr Ala Glu Glu Thr Tyr Pro Gly Lys Leu Leu Lys Ile Lys 720
 229 705 710 715 720
 231 Asp Arg Val Ser Glu Leu Met Pro Ser Ile Ser Gln Asp Ser Ile Thr 735
 232 725 730 735
 234 Val Ser Ala Asn Gln Tyr Glu Val Arg Ile Asn Glu Glu Gly Lys Arg 750
 235 740 745 750
 237 Glu Ile Leu Asp His Ser Gly Lys Trp Ile Asn Lys Glu Glu Ser Ile 765
 238 755 760 765
 240 Ile Lys Asp Ile Ser Ser Lys Glu Tyr Ile Ser Phe Asn Pro Lys Glu 780
 241 770 775 780
 243 Asn Lys Ile Ile Val Lys Ser Lys Tyr Leu His Glu Leu Ser Thr Leu 800
 244 785 790 795 800
 246 Leu Gln Glu Ile Arg Asn Ala Asn Ser Ser Asp Ile Asp Leu Glu 815
 247 805 810 815
 249 Lys Lys Val Met Leu Thr Glu Cys Glu Ile Asn Val Ala Ser Asn Ile 830
 250 820 825 830
 252 Asp Arg Gln Ile Val Glu Gly Arg Ile Glu Glu Ala Lys Asn Leu Thr 845
 253 835 840 845
 255 Ser Asp Ser Ile Asn Tyr Ile Lys Asn Glu Phe Lys Leu Ile Glu Ser 860
 256 850 855 860
 258 Ile Ser Asp Ser Leu Tyr Asp Leu Lys His Gln Asn Gly Leu Asp Asp 880
 259 865 870 875 880
 261 Ser His Phe Ile Ser Phe Glu Asp Ile Ser Lys Thr Glu Asn Gly Phe 895
 262 885 890 895
 264 Arg Ile Arg Phe Ile Asn Lys Glu Thr Gly Asn Ser Ile Phe Ile Glu 910
 265 900 905 910
 267 Thr Glu Lys Glu Ile Phe Ser Glu Tyr Ala Thr His Ile Ser Lys Glu 925
 268 915 920 925
 270 Ile Ser Asn Ile Lys Asp Thr Ile Phe Asp Asn Val Asn Gly Lys Leu 940
 271 930 935 940
 273 Val Lys Lys Val Asn Leu Asp Ala Ala His Glu Val Asn Thr Leu Asn 960
 274 945 950 955 960
 276 Ser Ala Phe Phe Ile Gln Ser Leu Ile Glu Tyr Asn Thr Thr Lys Glu 975
 277 965 970 975
 279 Ser Leu Ser Asn Leu Ser Val Ala Met Lys Val Gln Val Tyr Ala Gln 990
 280 980 985 990
 282 Leu Phe Ser Thr Gly Leu Asn Thr Ile Thr Asp Ala Ser Lys Val Val 1005
 283 995 1000 1005
 285 Glu Leu Val Ser Thr Ala Leu Asp Glu Thr Ile Asp Leu Leu Pro Thr

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286	1010	1015	1020
288	Leu Ser Glu Gly Leu Pro Ile Ile Ala Thr Ile Ile Asp Gly Val Ser		
289	1025	1030	1035
291	Leu Gly Ala Ala Ile Lys Glu Leu Ser Glu Thr Asn Asp Pro Leu Leu		1040
292	1045	1050	1055
294	Arg Gln Glu Ile Glu Ala Lys Ile Gly Ile Met Ala Val Asn Leu Thr		
295	1060	1065	1070
297	Ala Ala Ser Thr Ala Ile Val Thr Ser Ala Leu Gly Ile Ala Ser Gly		
298	1075	1080	1085
300	Phe Ser Ile Leu Leu Val Pro Leu Ala Gly Ile Ser Ala Gly Ile Pro		
301	1090	1095	1100
303	Ser Leu Val Asn Asn Glu Leu Ile Leu Gln Asp Lys Ala Thr Lys Val		
304	1105	1110	1115
306	Ile Asp Tyr Phe Lys His Ile Ser Leu Ala Glu Thr Glu Gly Ala Phe		1120
307	1125	1130	1135
309	Thr Leu Leu Asp Asp Lys Ile Ile Met Pro Gln Asp Asp Leu Val Leu		
310	1140	1145	1150
312	Ser Glu Ile Asp Phe Asn Asn Ser Ile Thr Leu Gly Lys Cys Glu		
313	1155	1160	1165
315	Ile Trp Arg Ala Glu Gly Gly Ser Gly His Thr Leu Thr Asp Asp Ile		
316	1170	1175	1180
318	Asp His Phe Phe Ser Ser Pro Ser Ile Thr Tyr Arg Lys Pro Trp Leu		
319	1185	1190	1195
321	Ser Ile Tyr Asp Val Leu Asn Ile Lys Lys Glu Lys Ile Asp Phe Ser		1200
322	1205	1210	1215
324	Lys Asp Leu Met Val Leu Pro Asn Ala Pro Asn Arg Val Phe Gly Tyr		
325	1220	1225	1230
327	Glu Met Gly Trp Thr Pro Gly Phe Arg Ser Leu Asp Asn Asp Gly Thr		
328	1235	1240	1245
330	Lys Leu Leu Asp Arg Ile Arg Asp His Tyr Glu Gly Gln Phe Tyr Trp		
331	1250	1255	1260
333	Arg Tyr Phe Ala Phe Ile Ala Asp Ala Leu Ile Thr Lys Leu Lys Pro		
334	1265	1270	1275
336	Arg Tyr Glu Asp Thr Asn Val Arg Ile Asn Leu Asp Gly Asn Thr Arg		1280
337	1285	1290	1295
339	Ser Phe Ile Val Pro Val Ile Thr Thr Glu Gln Ile Arg Lys Asn Leu		
340	1300	1305	1310
342	Ser Tyr Ser Phe Tyr Gly Ser Gly Gly Ser Tyr Ser Leu Ser Leu Ser		
343	1315	1320	1325
345	Pro Tyr Asn Met Asn Ile Asp Leu Asn Leu Val Glu Asn Asp Thr Trp		
346	1330	1335	1340
348	Val Ile Asp Val Asp Asn Val Val Lys Asn Ile Thr Ile Glu Ser Asp		
349	1345	1350	1355
351	Glu Ile Gln Lys Gly Glu Leu Ile Glu Asn Ile Leu Ser Lys Leu Asn		1360
352	1365	1370	1375
354	Ile Glu Asp Asn Lys Ile Ile Leu Asn Asn His Thr Ile Asn Phe Tyr		
355	1380	1385	1390
357	Gly Asp Ile Asn Glu Ser Asn Arg Phe Ile Ser Leu Thr Phe Ser Ile		
358	1395	1400	1405

VERIFICATION SUMMARY
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Input Set : A:\98502bet.app
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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date